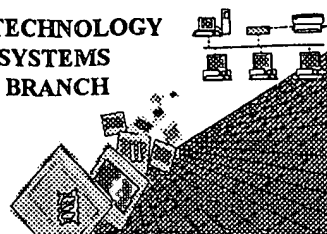


0590  
2520

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



RAW SEQUENCE LISTING  
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/994,227A  
Source: O/PE  
Date Processed by STIC: 5/29/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission  
User Manual - ePAVE)

2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/994,227A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences  
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences  
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIBE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/994,227A

DATE: 05/29/2002  
TIME: 15:06:26

Input Set : A:\407T-899210US.txt  
Output Set: N:\CRF3\05292002\I994227A.raw

*pp 1-3*  
Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: FOGELMAN, ALAN  
4 NAVAB, MOHAMMAD  
6 <120> TITLE OF INVENTION: CONTROL OF A GENE INDUCED BY OXIDIZED LIPIDS IN HUMAN ARTERY  
WALL CELLS  
8 <130> FILE REFERENCE: 407T-899210US  
10 <140> CURRENT APPLICATION NUMBER: US 09/994,227A  
11 <141> CURRENT FILING DATE: 2001-11-26  
13 <150> PRIOR APPLICATION NUMBER: US 09/539,569  
14 <151> PRIOR FILING DATE: 2000-03-31  
16 <160> NUMBER OF SEQ ID NOS: 3  
18 <170> SOFTWARE: PatentIn version 3.0  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 303  
22 <212> TYPE: DNA  
C--> 23 <213> ORGANISM: Artificial  
25 <220> FEATURE:  
26 <223> OTHER INFORMATION: Probe  
28 <400> SEQUENCE: 1  
29 gaatgtgctg agttcagcaa atgtcttgac gctaagtcac caccataact gcttagaaac 60  
31 ccagaggaac tcgggtgaag ttaaataaat aaggaccagc cctctcgagc ccctcccaga 120  
33 gttattgcat ttctcctctc aaggagcatg gaggccaat gggatgtgaa gagcctcacc 180  
35 tcccgaggcc ttccagcagc tgggagaggt cgtaatggg ctctgaaggt agctcagcgc 240  
37 actgttcgtg gaggggacag ggatggagac ggggaagttg aacacggtg tggtggaggt 300  
39 gct 303  
42 <210> SEQ ID NO: 2  
43 <211> LENGTH: 20  
44 <212> TYPE: DNA  
C--> 45 <213> ORGANISM: Artificial *insufficient explanation - give source of genetic material*  
47 <220> FEATURE:  
48 <223> OTHER INFORMATION: oligonucleotide *(see item 11 on Encl Summary sheet)*  
50 <400> SEQUENCE: 2  
51 ggaactcagt ggaactcagg 20  
54 <210> SEQ ID NO: 3  
55 <211> LENGTH: 14  
56 <212> TYPE: RNA  
C--> 57 <213> ORGANISM: Artificial  
59 <220> FEATURE:  
60 <223> OTHER INFORMATION: ribozyme sequence  
62 <220> FEATURE:  
63 <221> NAME/KEY: misc\_feature  
64 <222> LOCATION: (1)..(3)  
65 <223> OTHER INFORMATION: n is a, c, g, or u  
68 <220> FEATURE:  
69 <221> NAME/KEY: misc\_feature

## RAW SEQUENCE LISTING

DATE: 05/29/2002

PATENT APPLICATION: US/09/994,227A

TIME: 15:06:26

Input Set : A:\407T-899210US.txt

Output Set: N:\CRF3\05292002\I994227A.raw

70 <222> LOCATION: (9)..(13)  
71 <223> OTHER INFORMATION: n is a, c, g, or u  
74 <220> FEATURE:  
75 <221> NAME/KEY: misc\_feature  
76 <222> LOCATION: (5)..(5)  
77 <223> OTHER INFORMATION: n is a, c, g, or u  
80 <220> FEATURE:  
81 <221> NAME/KEY: misc\_feature  
82 <222> LOCATION: (4)..(4)  
83 <223> OTHER INFORMATION: b is c, g, or u  
86 <400> SEQUENCE: 3

*what about "n" at location 14?*

W--&gt; 87 nnnbngucnn nnnn

14

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/994,227A

DATE: 05/29/2002  
TIME: 15:06:27

Input Set : A:\407T-899210US.txt  
Output Set: N:\CRF3\05292002\I994227A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1,2,3,5,9,10,11,12,13,14

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3